

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 22, 2003, 15:14:29 ; Search time 42 seconds  
(without alignments)  
801.406 Million cell updates/sec

Title: US-09-745-506-37

Perfect score: 350

Sequence: 1 MDLKAISLNDFAISLFAE.....LENKINIILSTDRDPQGVV 350

Scoring table: OLIGO

Searched: 283308 seqs, 96168682 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database:

1: PIR76:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	2.9	366	2	F89936 conserved hypotet
2	9	2.6	288	2	S64243 hypothetical prote
3	8	2.3	262	2	C71109 hypothetical prote
4	8	2.3	445	2	F82176 agglutination prot
5	8	2.3	524	2	T36301 probable transcrip
6	7	2.0	97	2	T22871 hypothetical prote
7	7	2.0	104	2	B97047 hypothetical prote
8	7	2.0	107	2	AF1948 hypothetical prote
9	7	2.0	107	2	H83596 hypothetical prote
10	7	2.0	146	1	JC6173 single-stranded DN
11	7	2.0	148	2	JC6172 single-stranded DN
12	7	2.0	150	1	OTR05A cytochrome-c oxida
13	7	2.0	163	2	A72530 probable isoprenol
14	7	2.0	181	2	A70418 conserved hypotet
15	7	2.0	193	2	T05475 hypothetical prote
16	7	2.0	221	2	T52138 hypothetical prote
17	7	2.0	224	2	S54218 eukaryotic cap-bln
18	7	2.0	224	2	A36675 flag protein - yer
19	7	2.0	224	2	A41128 myogenin - human
20	7	2.0	232	2	AC0219 flagella basal bod
21	7	2.0	240	2	T46269 hypothetical prote
22	7	2.0	242	2	F30315 methyl viologen-re
23	7	2.0	249	2	D81954 conserved hypotet
24	7	2.0	249	2	G81011 conserved hypotet
25	7	2.0	250	2	D75054 hypothetical prote
26	7	2.0	253	2	US0595 rod-core linker po
27	7	2.0	253	2	AH1873 phycoobilisome rod-
28	7	2.0	254	2	T46367 hypothetical prote
29	7	2.0	255	2	AB2109 hypothetical prote

30	7	2.0	269	2	T45345 hypothetical prote
31	7	2.0	275	2	S59545 porin (clone Tava
32	7	2.0	278	2	T40916 ngli-interacting f
33	7	2.0	287	2	A31876 myogenin - rat
34	7	2.0	291	2	H71304 probable ribosomal
35	7	2.0	294	2	T33307 hypothetical prote
36	7	2.0	296	2	C95961 probable sugar up
37	7	2.0	312	1	R5BX0E acidic ribosomal p
38	7	2.0	314	2	E81064 tellurite resistan
39	7	2.0	330	2	F69471 atrazine chlorohyd
40	7	2.0	348	1	R5HS10 ribosomal protein
41	7	2.0	356	2	T51574 hypothetical prote
42	7	2.0	358	2	AD1830 GDP-mannose pyroph
43	7	2.0	381	2	A81307 thii protein C1104
44	7	2.0	396	2	S31151 translation elonga
45	7	2.0	431	2	C83858 5-enolpyruvylshik

#### ALIGNMENTS

```
RESULT 1
F89936
conserved hypothetical protein SAI388 [imported] - Staphylococcus aureus (strain N315
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: F89936
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-U, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MID:21311952; PMID:11418146
A:Accession: F89936
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-366 <RUR>
A:Cross-references: GB:BA000018; PID:g13701357; PIDN:BA842651.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAI388

Query Match 2.9%; Score 10; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 AESMDNVGILL 28
Db 19 AESMDNVGILL 28

RESULT 2
S64243
hypothetical protein YGL221c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G1020
C:Species: Saccharomyces cerevisiae
C>Date: 11-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
A:Accession: S64243
R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64071
A:Accession: S64243
A:Molecule type: DNA
A:Residues: 1-288 <RIE>
A:Cross-references: EMBL:Z72743; NID:g1322868; PIDN:CAA96937.1; PID:g1322869; MIPS:YG
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:NIF3
A:Cross-references: SGD:S0003189; MIPS:YGL221c
A:Map position: 7L
C:Superfamily: conserved hypothetical protein YGL144c

Query Match 2.6%; Score 9; DB 2; Length 288;
```

Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 312 HSNTERGFL 320  
|||||||  
DB 252 HSNTERGFL 260

## RESULT 3

C71109  
hypothetical protein PH0642 - *Pyrococcus horikoshii*  
C:Species: *Pyrococcus horikoshii*  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000  
C:Accession: C71109  
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
DNA Ref. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137; PMID:9679194  
A:Accession: C71109  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-262 <KAM>  
A:Cross-references: GB:AP000003; NID:g3236130; PIDN:BA29733.1; PID:g3257050  
A:Experimental source: strain 073  
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C:Genetics:  
A:Gene: PH0642  
C:Superfamily: hypothetical protein YLR351c

Query Match 2.3%; Score 8; DB 2; Length 262;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 IRLAENRV 94  
|||||||  
DB 183 IRLAENRV 190

## RESULT 4

F82176  
agglutination protein VC1621 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)  
C:Species: *Vibrio cholerae*  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
C:Accession: F82176  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F  
L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: F82176  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-445 <HEI>  
A:Cross-references: GB:AE004240; GB:AE003852; NID:g9656133; PIDN:AAF4774.1; GSPDB:GN001  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC1621  
A:Map position: 1

Query Match 2.3%; Score 8; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 SKAPNYPT 136  
|||||||  
DB 272 SKAPNYPT 279

## RESULT 5

T36301  
probable transcription regulator - *Streptomyces coelicolor*

C:Species: *Streptomyces coelicolor*  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 07-Dec-1999  
C:Accession: T36301  
R:Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M  
submitted to the EMBL Data Library, March 1999  
A:Reference number: 221604  
A:Accession: T36301  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-524 <SAU>  
A:Cross-references: EMBL:AL035654; PIDN:CAB38580.1; GSPDB:GN00070; SCOEDB:SC8.02  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCOEDB:SC8.02

Query Match 2.3%; Score 8; DB 2; Length 524;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 LDESYSIA 236  
|||||||  
DB 106 LDESYSIA 113

## RESULT 6

T22871  
hypothetical protein F5768.9 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T22871  
R:McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: 219630  
A:Accession: T22871  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-97 <WIL>  
A:Cross-references: EMBL:T283111; PIDN:CAB05530.1; GSPDB:GN00023; CESP:F5768.9  
A:Experimental source: clone F5768  
C:Genetics:  
A:Gene: CESP:F5768.9  
A:Map position: 5  
A:Introns: 5/3; 54/3

Query Match 2.0%; Score 7; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 SVTSFSA 172  
|||||||  
DB 90 SVTSFSA 96

## RESULT 7

B97047  
hypothetical protein CAC1193 [imported] - *Clostridium acetobutylicum*  
C:Species: *Clostridium acetobutylicum*  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: B97047  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L  
J. Bacteriol. 183, 4833-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: B97047  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-104 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK79165.1; PID:g15024115; GSPDB:GN00168  
A:Experimental source: *Clostridium acetobutylicum* ATCC824  
C:Genetics:  
A:Gene: CAC1193

Query Match 2.0%; Score 7; DB 2; Length 104;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 198 LSRNKL 204  
DB 58 LSRNKL 64

## RESULT 8

AF1948  
hypothetical protein alr1137 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AF1948  
R:Name: T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*  
A:Reference number: AB1807; MWID:21595285; PMID:11759840  
A:Accession: AF1948  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-107 <NR>  
A:Cross-references: GB:BA000019; PIDN:BA73094.1; PID:g17130483; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr1137

Query Match 2.0%; Score 7; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 194 VVDFLSR 200  
DB 33 VVDFLSR 39

## RESULT 9

AB3596  
hypothetical protein PA0385 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C:Species: *Pseudomonas aeruginosa*  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: AB3596  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.D.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin, N.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A:Reference number: AB2950; MWID:20437337; PMID:10984043  
A:Accession: AB3596  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-107 <STO>  
A:Cross-references: GB:AE004476; GB:AE004091; NID:g9946234; PIDN:AA03774.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0385

Query Match 2.0%; Score 7; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 WIAKGL 119  
DB 76 WIAKGL 82

## RESULT 10

JC6173  
single-stranded DNA-binding protein 1 precursor, mitochondrial - African clawed frog  
N:Alternate names: helix-destabilizing protein; single-stranded DNA-binding protein s

C:Species: *Xenopus laevis* (African clawed frog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: JC6173; S22300; S20262; S01116  
R:Chapman, A.M.; Dufresne, C.; Viney, L.; Gueride, M.  
Gene 184, 65-71, 1997  
A:Title: Cloning, sequencing and expression of the two genes encoding the mitochondrial  
A:Reference number: JC6172; MWID:97169147; PMID:9016954  
A:Contents: oocyte

A:Accession: JC6173

A:Molecule type: mRNA

A:Residues: 1-146 <CHA>

A:Cross-references: EMBL:X83673; NID:g620127; PIDN:CA58647.1; PID:g1890238

R:Ritanti, V.; Barot-Gueride, M.; Bilj, J.; DiDonato, S.; Zeviani, M.  
Nucleic Acids Res. 19, 4291, 1991

A:Title: A full-length cDNA encoding a mitochondrial DNA-specific single-stranded DNA

A:Reference number: S22300; MWID:91354145; PMID:1870981

A:Accession: S22300

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-146 <TR>

A:Cross-references: EMBL:X59285; NID:g64898; PIDN:CA41976.1; PID:g64899

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, April 1991

R:Ghir, R.; Lecae, J.P.; Dufresne, C.; Gueride, M.  
Arch. Biochem. Biophys. 291, 395-400, 1991

A:Title: Primary structure of the two variants of *Xenopus laevis* mtSSB, a mitochondrial

A:Reference number: S20262; MWID:92061073; PMID:1952953

A:Accession: S20262

A:Molecule type: protein

A:Residues: 18-142 <GHR>

R:Mahongou, C.; Ghir, R.; Lecae, J.P.; Mignotte, B.; Barot-Gueride, M.  
FEBS Lett. 235, 267-270, 1988

A:Title: The amino-terminal sequence of the *Xenopus laevis* mitochondrial SSB is homologous to the

A:Reference number: S01116; MWID:88296837; PMID:3042458

A:Accession: S01116

A:Molecule type: protein

A:Residues: 18-26, 'E', '28-41 <MAH>

A:Comment: This protein is essential for replication, repair of recombination. It is involved, and it modulates the level of replication and transcription mediated by mitochondrial

C:Genetics:

A:Gene: ssb2

A:Genome: nuclear

A:Insertions: 8/3; 27/1; 74/1; 104/2; 134/1

C:Superfamily: single-stranded DNA-binding protein; single-stranded DNA-binding protein; tetr

C:Keywords: DNA replication; mitochondrion; oocyte; single-stranded DNA binding; tetr

F:1-17/Domain: transit peptide (mitochondrion) #status predicted <TMP>

F:18-16/Product: single-stranded DNA-binding protein 1 #status predicted <MAT>

F:44-129/Domain: single-stranded DNA-binding protein homology <SSD>

Query Match 2.0%; Score 7; DB 1; Length 146;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 319 FLSDLRD 325  
DB 138 FLSDLRD 144

## RESULT 11

JC6172  
single-stranded DNA-binding protein 2 precursor, mitochondrial - African clawed frog  
N:Alternate names: helix-destabilizing protein; single-stranded DNA-binding protein r  
C:Species: *Xenopus laevis* (African clawed frog)  
C:Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 20-Jun-2000  
C:Accession: JC6172; S20263; S01117  
R:Chapman, A.M.; Dufresne, C.; Viney, L.; Gueride, M.  
Gene 184, 65-71, 1997  
A:Title: Cloning, sequencing and expression of the two genes encoding the mitochondrial  
A:Reference number: JC6172; MWID:97169147; PMID:9016954  
A:Accession: JC6172  
A:Molecule type: mRNA  
A:Residues: 1-148 <CHA>  
A:Cross-references: EMBL:X83674; NID:g620128; PIDN:CA58648.1; PID:g1890239

A:Experimental source: cocycle  
 R:Ghrir, R.; Lecaer, J.P.; Dufresne, C.; Gueride, M.  
 Arch. Biochem. Biophys. 291, 395-400, 1991  
 A:Title: Primary structure of the two variants of Xenopus laevis mtSSB, a mitochondrial  
 A:Reference number: S20262; MUID:92061073; PMID:1952955  
 A:Accession: S20263  
 A:Molecule type: protein  
 A:Residues: 18-48, 'E', 50-99 <GHR>  
 R:Monthougon, C.; Ghrir, R.; Lecaer, J.P.; Mignotte, B.; Barat-Gueride, M.  
 FEBS Lett. 235, 267-270, 1988  
 A:Title: The amino-terminal sequence of the Xenopus laevis mitochondrial SSB is homologous  
 A:Reference number: S01116; MUID:88296837; PMID:3042458  
 A:Accession: S01117  
 A:Molecule type: protein  
 A:Residues: 18-22, 'X', 24-28, 'X', 30-38 <MAH>  
 C:Comment: This protein is essential for replication, repair of recombination. It is coded, and it modulates the level of replication and transcription mediated by mitochondrial  
 C:Comment: This protein binds preferentially to single-stranded DNA.  
 C:Genetics:  
 A:Gene: ssb1  
 A:Genome: nuclear  
 A:Insertions: 8/3; 29/1; 76/1; 106/2; 136/1  
 C:Superfamily: single-stranded DNA-binding protein; single-stranded DNA-binding protein  
 C:Keywords: DNA replication; mitochondrion; cocycle; single-stranded DNA binding  
 F:1-17/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
 F:18-148/Product: single-stranded DNA-binding protein 2 #status experimental <MAT>  
 F:46-131/Domain: single-stranded DNA-binding protein homology <SSD>

Query Match 2.0%; Score 7; DB 2; Length 148;  
 Best Local Similarity 100.0%; Pred. No. 41;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 FLSDLRD 325  
 |||||  
 DB 140 FLSDLRD 146

RESULT 12  
 OTHD5A  
 cytochrome-c oxidase (EC 1.9.3.1) chain Va precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Jun-1999  
 C:Accession: J0342  
 R:Rizuto, R.; Nakase, H.; Zeviani, M.; DiMauro, S.; Schon, E.A.  
 Gene 69, 245-256, 1988  
 A:Title: Subunit Va of human and bovine cytochrome c oxidase is highly conserved.  
 A:Reference number: J0342; MUID:89172069; PMID:2853101  
 A:Accession: J0342  
 A:Molecule type: mRNA  
 A:Residues: 1-150 <RTZ>  
 A:Cross-references: GB:M22760; NID:g695359; PIDD:AAA99220.1; PID:g695360  
 C:Genetics:  
 A:Gene: COX5A  
 A:Genome: nuclear  
 C:Complex: part of a 13 chain complex spanning the inner mitochondrial membrane and cons  
 m dmers within the mitochondrial inner-membrane  
 C:Function:  
 A:Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecule  
 ns from the mitochondrial matrix producing two molecules of water and lowering the conce  
 A:Pathway: oxidative phosphorylation; respiratory chain  
 A>Note: the role of chain Va is not clear  
 C:Superfamily: mammalian cytochrome-c oxidase chain Va  
 C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane  
 F:1-41/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
 F:42-150/Product: cytochrome-c oxidase chain Va #status predicted <MAT>  
 F:42-150/Domain: mitochondrial matrix #status predicted <MM1>

Query Match 2.0%; Score 7; DB 1; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LNDPASTL 16

Db 99 LNDPASTL 105  
 |||||

RESULT 13  
 A72530  
 Probable Isocitrate dehydrogenase alpha subunit APE213 - Aeropyrum pernix (stra  
 C:Species: Aeropyrum pernix  
 C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 28-Jul-2000  
 C:Accession: A72530  
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta  
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.  
 DNA Res. 6, 83-101, 1999  
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero  
 A:Reference number: A72450; MUID:99310339; PMID:10382966  
 A:Accession: A72530  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-163 <KAM>  
 A:Cross-references: DDBJ:AP000063; NID:g5105654; PIDD:BA81225.1; PID:g5105913  
 A:Experimental source: strain KI  
 C:Genetics:  
 A:Gene: APE213  
 C:Superfamily: isocitrate dehydrogenase alpha chain; ferredoxin [2Fe-2S] homolog  
 C:Keywords: 2Fe-2S; metalloprotein  
 F:30-68/Domain: ferredoxin [2Fe-2S] homology <FDX>  
 F:47,52,55,67/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 2.0%; Score 7; DB 2; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 DFLSRNK 202  
 |||||  
 DB 119 DFLSRNK 125

RESULT 14  
 A70418  
 conserved hypothetical protein aq\_1359 - Aquifex aeolicus  
 C:Species: Aquifex aeolicus  
 C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
 C:Accession: A70418  
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;  
 V.  
 Nature 392, 353-358, 1998  
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A:Reference number: A70300; MUID:98196666; PMID:9537320  
 A:Accession: A70418  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-181 <AQF>  
 A:Cross-references: GB:AE000736; NID:g2983763; PIDD:MAC07339.1; PID:g2983780; GB:AE00  
 A:Experimental source: strain VP5  
 C:Genetics:  
 A:Gene: aq\_1359

Query Match 2.0%; Score 7; DB 2; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 LVTRALE 91  
 |||||  
 DB 97 LVTRALE 103

RESULT 15  
 T05475  
 hypothetical protein T805.140 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 23-Jul-1999  
 C:Accession: T05475  
 R:Bevan, M.; Wedler, H.; Wamboldt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schue

submitted to the Protein Sequence Database, February 1998

A:Reference number: 215417

A:Accession: T05475

A:Molecule type: DNA

A:Residues: 1-193 <BEV>

A:Cross-references: EMBL:AL021890

A:Experimental source: cultivar Columbia; BAC clone T805

C:Genetics:

A:Map position: 4

A:Introns: 5/3

A>Note: T805.140

Query Match

Best Local Similarity 2.0%; Score 7; DB 2; Length 193;  
100.0%; Pred. No. 53;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LGVGRRL 261

DB 167 LGVGRRL 173

Search completed: August 22, 2003, 15:20:16  
Job time : 55 secs

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